`Blast 2 Sequence;

Exhibit 3

| NCBI | Entrez | BLAST 2 sequences | BLAST | Example | Help |

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for
comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastn ▼ Matrix Not Applicable ▼

Parameters used in BLASTN program only:
Reward for a match: 1   **Penalty for a mismatch:** -2
☐ Use Mega BLAST Strand option Both strands ▼

Open gap 5 and extension gap 2 penalties
gap x_dropoff 5) expect 10 word size 11 Filter ☑

Sequence 1 Enter accession or GI 13027635 or download from file [_____] Browse
or sequence in FASTA format from: [_____] to: [_____]

[_____]

Sequence 2 Enter accession or GI [_____] or download from file [_____] Browse
or sequence in FASTA format from: [_____] to: [_____]

cgaccaagtctac agcgcttccggt

[Align] [Clear Input]

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov
Credits to: Tatiana Tatusov and Tom Madden

˙ Blast Result

Blast 2 Sequences results

PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   Align

Sequence 1	gi 130 7635	Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA	Length 2753
Sequence 2	lcl|seq_2		Length 25

No significant similarity was found